

Serial Number: 08/819, 069E

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1648

#159

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☒ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: 8,24
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: Seq 17, 27 - replaced ; w/ colon

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/819,669EDATE: 07/14/2000
TIME: 22:45:27

INPUT SET: S35683.raw

<p>This Raw Listing contains the General Information Section and up to the first 5 pages.</p>

SEQUENCE LISTING

(1) General Information:

- (i) APPLICANTS: Boon-Falleur, Thierry; Van der Bruggen, Thierry;
Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
- (ii) TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
Rejection Antigens and Uses Thereof
- (iii) NUMBER OF SEQUENCES: 28
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Fulbright & Jaworski LLP
(B) STREET: 666 Fifth Avenue
(C) CITY: New York City
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10103
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
(B) COMPUTER: IBM
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/819,669
(B) FILING DATE: 17-March-1997
(C) CLASSIFICATION: 435
- (vii) PRIOR APPLIATION DATA:
(A) APPLICATION NUMBER: 08/142,368
(B) FILING DATE: 02-MAY-1994
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/US92/04354
(B) FILING DATE: 22-MAY-1992
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 07/807,043
(B) FILING DATE: 12-DECEMBER-1991
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 07/764,364

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PATENT APPLICATION US/08/819,669EDATE: 07/14/2000
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47 (B) FILING DATE: 23-SEPTEMBER-1991

48

49 (vii) PRIOR APPLICATION DATA:

50 (A) APPLICATION NUMBER: 07/728,838

51 (b) FILING DATE: 9-JULY-1991

52

53 (vii) PRIOR APPLICATION DATA:

54 (A) APPLICATION NUMBER: 07/705,702

55 (B) FILING DATE: 23-May-1991

56

57 (viii) ATTORNEY/AGENT INFORMATION:

58 (A) NAME: Hanson, Norman D.

59 (B) REGISTRATION NUMBER: 30,946

60 (C) REFERENCE/DOCKET NUMBER: LUD 5253.5-US

61

62 (ix) TELECOMMUNICATION INFORMATION:

63 (A) TELEPHONE: (212)318-3168

64 (B) TELEFAX: (212)752-5958

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68 (2) INFORMATION FOR SEQ ID NO: 1:

69 (i) SEQUENCE CHARACTERISTICS:

70 (A) LENGTH: 462 base pairs

71 (B) TYPE: nucleic acid

72 (C) STRANDEDNESS: single

73 (D) TOPOLOGY: linear

74 (ii) MOLECULE TYPE: genomic DNA

75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

76

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80 ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG 60

81 ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTT 120

82 CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG 180

83 CTTGTGAATT TGTACCCCTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC 240

84 CCCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300

85 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG CATGCATTGT 360

86 GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT 420

87 TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC 462

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89

90

91 (2) INFORMATION FOR SEQ ID NO: 2:

92 (i) SEQUENCE CHARACTERISTICS:

93 (A) LENGTH: 675 base pairs

94 (B) TYPE: nucleic acid

95 (C) STRANDEDNESS: single

96 (D) TOPOLOGY: linear

97 (ii) MOLECULE TYPE: genomic DNA

98 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

99

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100
101 ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT 48
102 Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
103          5          10          15
104 GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA 96
105 Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
106          20          25          30
107 GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA 144
108 Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
109          35          40          45
110 AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG 192
111 Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
112          50          55          60
113 TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC 240
114 Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser
115          65          70          75          80
116 TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC 288
117 Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr
118          85          90          95
119 GAC GAC GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 336
120 Asp Asp Glu Asp Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp
121          100          105          110
122 GAG GAA GAA GAA TTG GAG AAC CTC ATG GAT GAT GAA TCA GAA GAT GAG 384
123 Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu
124          115          120          125
125 GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG 432
126 Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met
127          130          135          140
128 GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG 480
129 Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys
130          145          150          155          160
131 AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC CAC GAC CCT AAT TTC 528
132 Asn Glu Val Lys Cys Arg Met Ile Tyr Phe His Asp Pro Asn Phe
133          165          170          175
134 CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT 576
135 Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys
136          180          185          190
137 GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG 624
138 Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu Glu
139          195          200          210
140 GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT 672
141 Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro
142          220          225          230          235
143
144 TAG 675
145
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147

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(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTTT 60
TTCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA ATTTGATTTT GTTCTAAAGT 120
TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTGCAT GGTGAACCTT CATATGATAC 180
ATAGGATTAC ACTTGTACCT GTTAAAAATA AAAGTTTGAC TTGCATAC 228

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1365 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT 50
GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT 100
CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG 150
AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT 200
CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA 250
CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCAG 350
CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG 400
CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT 450
ACCCTTTGTG CC 462
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA 504
GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG 546
TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC 588
TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC 630
ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC 672
TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG 714
GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC 756
GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 798
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA 840
GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA 882
GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT 924
GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT 966
TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG 1008
AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT 1050
GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG GAG GAG 1092
GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT 1134
TAG 1137
GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG 1187
TTGTTTTTTT TTCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA 1237
ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT 1287

RAW SEQUENCE LISTING PATENT APPLICATION US/08/819,669E

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206 CTGACTGCAT GGTGAACTTT CATATGATAC ATAGGATTAC ACTTGACCT 1337
207 GTTAAAAATA AAAGTTTGAC TTGCATAC 1365

208
209
210

211 (2) INFORMATION FOR SEQ ID NO: 5:

212 (i) SEQUENCE CHARACTERISTICS:

213 (A) LENGTH: 4698 base pairs

214 (B) TYPE: nucleic acid

215 (C) STRANDEDNESS: single

216 (D) TOPOLOGY: linear

217 (ii) MOLECULE TYPE: genomic DNA

218 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

219

220 ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT 50
221 GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT 100
222 CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG 150
223 AAGTTTTGCA AGTTCCGCTT ACAGCTCTAG CTTGTGAATT TGTACCCTTT 200
224 CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA 250
225 CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
226 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCAG 350
227 CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG 400
228 CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT 450
229 ACCCTTTGTG CC 462
230 ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA 504
231 GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG 546
232 TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC 588
233 TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC 630
234 ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC 672
235 TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG 714
236 GAT GAA GAC GAT GAG GAT GAT GAT GAT GAC TAC TAC GAC GAC 756
237 GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 798
238 GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA 840
239 GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA 882
240 GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T 916
241 GTGAGTAACC CGTGGTCTTT ACTCTAGATT CAGGTGGGGT GCATTCTTTA 966
242 CTCTTGCCCA CATCTGTAGT AAAGACCACA TTTTGGTTGG GGGTCATTGC 1016
243 TGGAGCCATT CCTGGCTCTC CTGTCCACGC CTATCCCCGC TCCTCCCATC 1066
244 CCCCACCTCT TGCTCCGCTC TCTTTCTTTT TCCCACCTTG CCTCTGGAGC 1116
245 TTCAGTCCAT CCTGCTCTGC TCCCTTTCCC CTTTGCTCTC CTTGCTCCCC 1166
246 TCCCCCTCGG CTCAACTTTT CGTGCCTTCT GCTCTCTGAT CCCCACCCTC 1216
247 TTCAGGCTTC CCCATTTGCT CCTCTCCCGA AACCTCCCC TTCCTGTTCC 1266
248 CCTTTTCGCG CCTTTTCTTT CCTGCTCCCC TCCCCCTCCC TATTTACCTT 1316
249 TCACCAGCTT TGCTCTCCCT GCTCCCCCTC CCCTTTTGCA CCTTTTCTTT 1366
250 TCCTGCTCCC CTCCCCCTCC CCTCCCTGTT TACCCTTCAC CGCTTTTCCT 1416
251 CTACCTGCTT CCCTCCCCCT TGCTGCTCCC TCCCTATTTG CATTTTCTGGG 1466
252 TGCTCCTCCC TCCCCCTCCC CCTCCCTCCC TATTTGCATT TTCGGGTGCT 1516
253 CCTCCCTCCC CCTCCCCAGG CCTTTTTTTT TTTTTTTTTT TTTTTTTTTT 1566
254 TTGGTTTTTC GAGACAGGGT TTCTCTTGT ATCCCTGGCT GTCCTGGCAC 1616
255 TCACTCTGTA GACCAGGCTG GCCTCAAAC CAGAAATCTG CCTGCCTCTG 1666
256 CCTCCCAAAT GCTGGGATTA AAGGCTTGCA CCAGGACTGC CCCAGTGCAG 1716
257 GCCTTTCTTT TTTCTCTCT CTGGTCTCCC TAATCCCTTT TCTGCATGTT 1766
258 AACTCCCTT TTGGCACCTT TCCTTTACAG GACCCCTCC CCCTCCCTGT 1816

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/819,669E

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Line	Error	Original Text
31	Wrong Classification	(C) CLASSIFICATION: 435